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REMARKS

Initially, Applicants thank the Examiner for returning a duly initialed copy of the Forms PTO-1449 with the Office Action, indicating consideration of the documents cited in the Information Disclosure Statements filed July 17, 2000 and September 14, 2000.

Applicants respectfully request that the Examiner acknowledge the claim of priority to Japanese Application No. 269611/1997, filed October 2, 1997, and the receipt of certified copies of the priority document in the next communication from the PTO. A verified English language translation of this document is provided herewith.

Reconsideration and withdrawal of the rejections of record are respectfully requested.

Summary of Status of Amendments and Office Action

In the present amendment, claims 1-4, 7 and 11 are amended and claims 12-20 are added. Therefore, claims 1-20 are pending in the application with claim 1 being independent.

In the Office Action, the specification was objected to objected to for use of improper language and format in the abstract.

Claims 1-10 are rejected under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 11 is rejected under 35 U.S.C. § 101 as being directed to non-statutory subject matter.

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Claims 1-8, 10 and 11 are rejected under 35 U.S.C. § 102(a) as being anticipated by Bystroff et al. (J. Molec. Biol., 1998, vol. 281, pp 565-577).

Claims 9-10 are rejected under 35 U.S.C. § 103(a) as being unpatentable over Bystroff et al. in view of Luthy et al. (Nature, 1992, vol. 356, pp 83-85).

Explanation and Support for Amendments

Applicants submit that each of the foregoing amendments is fully supported by the specification, *e.g.* pages 15, 18-19. Further, many of the amendments are in conformance with the Examiner's suggestions.

Response to Objections

Applicants note that the current amendments to the abstract avoids use of the terms "means" and "said," and more clearly and concisely discloses the invention. Thus, it is respectfully requested that the Examiner withdraw the objection to the specification.

Response to §112, second paragraph Rejections

Applicants note that the amendments to claim 1 incorporate the Examiner's suggestions made in the rejection under §112, second paragraph. Applicants note that the term "known or predicted" has been changed to "predetermined" in accordance with the Examiner's suggestion to advance prosecution on the merits, and is not intended to change the scope of the claim. Additionally, claim 1 now recites a final step to complete the claimed method.

With respect to the rejection of claim 2 as indefinite for use of the phrase "based on the three-dimensional structure of the reference protein," the language has been amended in accordance with the specification, page 15, to recite that the reference proteins are divided into two or more segment sequences based upon the characteristics of their three-dimensional structure.

With respect to the rejection of claim 3 as indefinite for use of the phrase "core segment sequences which substantially participate in the formation," the language has been amended to reflect that the core segment sequences include those amino acid residues predetermined to form a hydrophobic core.

With respect to the rejection of claim 4 as indefinite for use of the phrase "matching is conducted based on the information on the degree of burial into the inside of the protein," the claim has been modified in accordance with page 18 of the specification, to show that the information is the degree of burial or exposure of the side chains of the amino acids.

With respect to the rejection of claim 7 as indefinite for the asserted redundancy of step (b), Applicants respectfully submit that step (a) is directed to sliding "core segment sequences" whereas step (b) is directed to sliding "sub segment sequences." As the specification makes clear on page 19, "the matching is carried out in two steps by separating core segment sequences and sub segment sequences." Therefore, step (b) is not redundant of step (a) as they are directed to different sequences.

For the foregoing reasons, Applicants respectfully request that the Examiner withdraw the rejections of claims 1-11 under 35 U.S.C. § 112, second paragraph. The foregoing amendments have been made solely for the purpose of clarifying the claim language, and no estoppel should attach.

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Response to § 101 Rejection

Claim 11 is rejected under 35 U.S.C. § 101 as being directed to non-statutory material. The Office Action asserts that a database "does not extend the computer's capability to produce a useful result." In response, Applicants have amended claim 11 to recite the database is in computer readable form and new claims 12-20 also contain this new language.. The claimed database is used in the method of claims 1-10, and thus "extend[s] the computer's capability to produce a useful result."

Applicants therefore, respectfully request that the Examiner withdraw the rejection of claim 11 under 35 U.S.C. § 101.

Response to § 102(a) Rejection

Claims 1-8, 10 and 11 are rejected under 35 U.S.C. § 102(a) as being anticipated by Bystroff et al. The Office Action asserts that Bystroff et al. teaches a computerized method of predicting local structure in proteins using a library of sequence-structure motifs (or three dimensional databases). It is asserted that the method employs segmentation analysis comprising eight residue segments and involves confidence scoring.

In response, Applicants are submitting herewith a verified English language translation of Japanese Application No. 269611/1997, filed October 2, 1997. In this regard, Applicants note that their application is a national stage application of PCT/JP98/04557 filed October 2, 1998 and claims priority of Japanese Application No. 269611/1997. The verified translation renders the rejection

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under § 102(a) moot because it shows that Applicants invented the claimed subject matter before August 21, 1998, the publication date of Bystroff et al.

Applicants also wish to point out that Bystroff et al. does not disclose or suggest using information about amino acid residue side chains to develop the three-dimensional structure of a query protein. Thus, Bystroff et al. does not, and cannot anticipate Applicants claimed invention. Therefore, in view of the above Applicants respectfully request that the Examiner withdraw the rejection of claims 1-8, 10 and 11 under 35 U.S.C. § 102(a).

Response to § 103(a) Rejection

Claims 9 and 10 are rejected under 35 U.S.C. § 103(a) as unpatentable over Bystroff et al. in view of Luthy et al. The Office Action asserts that Luthy et al. discloses a method of self matching normalization, and one of ordinary skill in the art using Luthy et al. would have been motivated to use Bystroff et al. to make the claimed invention.
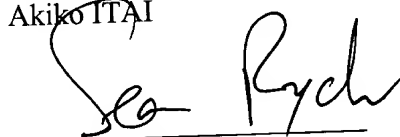
For the reasons given above, Applicants have both removed Bystroff et al. from the prior art, and pointed out the differences between Bystroff et al.'s teachings and Applicants claimed invention. Therefore Applicants respectfully request that the Examiner withdraw the rejection of claims 9-10 under 35 U.S.C. § 103(a).

CONCLUSION

For the reasons advanced above, Applicants respectfully submit that all pending claims patentably define Applicants' invention. Allowance of the application with an early mailing date of the Notices of Allowance and Allowability is therefore respectfully requested.

Should the Examiner have any further comments or questions, the Examiner is invited to contact the undersigned at the below-listed telephone number.

Respectfully submitted,
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MARKED UP COPY OF AMENDED SPECIFICATION

Please replace the Abstract with the following,

A method of predicting a scaffold of a protein comprising a query sequence, [wherein said method uses] using a database which contains environmental information on the side chain of each amino acid residue contained in the amino acid sequence of each reference protein whose three-dimensional structure is known or predictable, and [wherein said method comprises] comprising [the step of]: conducting matching based on the environmental information [on] of each amino acid residue of each reference protein and hydrophobicity or hydrophilicity property of the side chain of each amino acid residue of the query sequence, [and] choosing at least one template protein among the reference proteins that has high similarity in three-dimensional structure to the protein comprising the query sequence, and predicting the scaffold of the protein comprising a query sequence.

MARKED UP COPY OF AMENDED CLAIMS

1. (Amended Marked Up Copy) A method of predicting a scaffold of a protein comprising a query sequence, wherein said method uses a database which contains environmental information on the side chain of each amino acid residue contained in the amino acid sequence of each reference protein whose three-dimensional structure is [known or predictable] predetermined, and wherein said method comprises [the step of]: conducting matching based on the environmental information [on] of each amino acid residue of each reference protein and hydrophobicity or hydrophilicity property of the side chain of each amino acid residue of the query sequence, [and] choosing at least one protein as a template protein [among] from the reference proteins that has high similarity in three-dimensional structure to the protein comprising the query sequence, and predicting the scaffold of the protein comprising a query sequence.

2. (Amended Marked Up Copy) The method according to claim 1, wherein the amino acid sequence of each of the reference proteins is divided into two or more segment sequences comprising two or more continuous amino acid residues based on the characteristics of the three-dimensional structure of the reference protein.

3. (Amended Marked Up Copy) The method according to claim 2, wherein the amino acid sequence of each of the reference proteins is divided into one or more core segment sequences which are predetermined to form a [substantially participate in the formation of] hydrophobic core, and into one or more sub segment sequences which are not predetermined to form a [do not substantially participate in the formation of] hydrophobic core.

4. (Amended Marked Up Copy) The method according to claim 1, wherein the matching is conducted based on the information on degree of burial into the inside <u>of the protein of the side chain of each amino acid residue in the reference protein,</u> or degree of exposure to the protein surface of the side chain of each amino acid residue in the reference protein, together with the properties of hydrophobicity or hydrophilicity of each amino acid residue in the query sequence.

7. (Amended Marked Up Copy) The method according to claim 1, wherein the matching comprises [the steps of]: [(a) the step of] matching by sliding one or more core segment sequences on the query sequence, optionally considering gaps at one end or both ends of the core segment sequences, provided when two or more core segment sequences are used, the core segment sequences are placed in the order of appearance on the amino acid sequence of the reference protein; and, [(b) subsequent to the above step (a), the step of] sliding one or more sub segment sequences on the query sequence, optionally considering one or more gaps.

11.(Amended Marked Up Copy) A database <u>in a computer readable medium</u> which contains environmental information on the side chains of amino acid residues of one or more reference proteins with [known or predictable] <u>predetermined</u> three-dimensional structures, and which is used for the method according to claim 1.